



Alignment of human (query 1) and hamster (Sbjvt 1) SKI-1/S1P

Query: 1 MKLVNIWLLLLLVLLCGKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYIYIVAF 60
MKL+NIWLLLLLVLLCGKKHLGDRL KK+FEKA CP CSHLTLKVEFSSTVVEYIYIVAF
Sbjct: 1 MKLINIWLLLLLVLLCGKKHLGDRLGKKAFAKASCPCSHLTLKVEFSSTVVEYIYIVAF 60

Query: 61 NGYFTAKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSPDFEVIQIKEKQKAGLLTLEDH 120
NGYFTAKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSPDFEVIQIKEKQKAGLLTLEDH
Sbjct: 61 NGYFTAKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSPDFEVIQIKEKQKAGLLTLEDH 120

Query: 121 PNIKRVTQQRKVFRLSLKYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSFVHATGRH 180
PNIKRVTQQRKVFRLSLK+AESDP VPCNETRWSQKWQSSRPLRRASLSLGSFVHATGRH
Sbjct: 121 PNIKRVTQQRKVFRLSLKFAESDPIVPCNETRWSQKWQSSRPLRRASLSLGSFVHATGRH 180

Query: 181 SSRLLRAIPRQVAQTLQADVWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNE 240
SSRLLRAIPRQVAQTLQADVWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNE
Sbjct: 181 SSRLLRAIPRQVAQTLQADVWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNE 240

Query: 241 RTLDDGLGHGTFVAGVIASMRCCQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNAILKK 300
RTLDDGLGHGTFVAGVIASMRCCQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNAILKK
Sbjct: 241 RTLDDGLGHGTFVAGVIASMRCCQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNAILKK 300

Query: 301 IDVLNLSIGGPDFMDHPFVDKVVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGG 360
IDVLNLSIGGPDFMDHPFVDKVVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGG
Sbjct: 301 IDVLNLSIGGPDFMDHPFVDKVVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGG 360

Query: 361 IDFEDNIARFSSRGMTTWELPGGYGRMKPDIIVTYGAGVRGSGVKGGCRALSGTSVASPVV 420
IDFEDNIARFSSRGMTTWELPGGYGR+KPDIVTYGAGVRGSGVKGGCRALSGTSVASPVV
Sbjct: 361 IDFEDNIARFSSRGMTTWELPGGYGRVKPDIIVTYGAGVRGSGVKGGCRALSGTSVASPVV 420

Query: 421 AGAVTLLVSTVQKRELVPASMKQALIASARRLPVNMFEQGHGKLDLLRAYQILNSYKP 480
AGAVTLLVSTVQKRELVPAS+KQALIASARRLPVNMFEQGHGKLDLLRAYQIL+SYKP
Sbjct: 421 AGAVTLLVSTVQKRELVPASVKQALIASARRLPVNMFEQGHGKLDLLRAYQILSSYKP 480

Query: 481 QASLSPSYIDLTECPYMWPYCSQPIYYGGMPTVVNVITILNMGVGTGRIVDKPDWQPYLPQ 540
QASLSPSYIDLTECPYMWPYCSQPIYYGGMPT+VNVITILNMGVGTGRIVDKP+W+PYLPQ
Sbjct: 481 QASLSPSYIDLTECPYMWPYCSQPIYYGGMPTIVNVITILNMGVGTGRIVDKPEWRPYLPQ 540

Query: 541 NGDNIEVAFSYSSVLWPWSGYLAISISVTKKAASWEGIAQGHVMITVASPAETESKNGAE 600
NGDNIEVAFSYSSVLWPWSGYLAISISVTKKAASWEGIAQGH+MITVASPAETE+KNGAE
Sbjct: 541 NGDNIEVAFSYSSVLWPWSGYLAISISVTKKAASWEGIAQGHIMITVASPAETEAKNGAE 600

Query: 601 QTSTVKLPIKVKIIPTPPRSKRVLWDQYHNLRYPPGYFPRDNLRMKNDPLDWNVDHHTN 660
TSTVKLPIKVKIIPTPPRSKRVLWDQYHNLRYPPGYFPRDNLRMKNDPLDWNVDH+HTN
Sbjct: 601 HTSTVKLPIKVKIIPTPPRSKRVLWDQYHNLRYPPGYFPRDNLRMKNDPLDWNVDHVHTN 660

Query: 661 FRDMYQHLRSMGYFVEVLGAPFTCFDASQYGTLLMVDSEEEYFPEEIAKLRRDNDNGLSL 720
FRDMYQHLRSMGYFVEVLGAPFTCFDA+QYGTLLMVDSEEEYFPEEIAKLRRDNDNGLSL
Sbjct: 661 FRDMYQHLRSMGYFVEVLGAPFTCFDATQYGTLLMVDSEEEYFPEEIAKLRRDNDNGLSL 720

Query: 721 VIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFSDGLYEGEFTL 780
VIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFSDGLYEGEF L
Sbjct: 721 VIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFSDGLYEGEFAL 780

Query: 781 ANHDMYYASGCSIAKFPEDGVVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAEGGGR 840

Sbjct: 781 ANHDMYYASGCSIAKFPEDGVVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAEGGGR 840

Query: 841 IVLYGDSNCLDDSHRQKDCFWLLDALLQYTSYGVTPPSLSHSGNRQRPPSGAGSVTPERM 900
IVLYGDSNCLDDSHRQKDCFWLLDALLQYTSYGV PPSLSHSGNRQRPPSGAG PERM

Sbjct: 841 IVLYGDSNCLDDSHRQKDCFWLLDALLQYTSYGVNPPSLSHSGNRQRPPSGAGLAPPERM 900

Query: 901 EGNHLHRYSKVLEAHLGDPKPRPLPACPRLSWAKPQPLNETAPSNLWKHQKLLSIDLDKV 960
EGNHLHRYSKVLEAHLGDPKPRPLPACP LSWAKPQPLNETAPSNLWKHQKLLSIDLDKV

Sbjct: 901 EGNHLHRYSKVLEAHLGDPKPRPLPACPHLSWAKPQPLNETAPSNLWKHQKLLSIDLDKV 960

Query: 961 VLPNFRSNRPQVRPLSPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMVVLAFFVVQ 1020
VLPNFRSNRPQVRPLSPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMV LAFFVVQ

Sbjct: 961 VLPNFRSNRPQVRPLSPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMVALAFFVVQ 1020

Query: 1021 INKAKSRPKRRRPRAKRPQLMQQVHPPKTPSV 1052
I+KAKSRPKRRRPRAKRPQL QQ HPP+TPSV

Sbjct: 1021 ISKAKSRPKRRRPRAKRPQLTQQTHPPRTPSV 1052